

Sequence Alignment for 10/561,132

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US-10-120-604-101
; Sequence 101, Application US/10120604
; Patent No. 7049096
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN
COUPLED RECEPTORS,
; TITLE OF INVENTION: HGPRBMY28 AND HGPRBMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-101

Query Match          100.0%; Score 1813; DB 3; Length 986;
Best Local Similarity 100.0%; Pred. No. 3.4e-172;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TSFSILMSPDSPDPSSLLGILLDIISYVGVGFSILSLAACLVVEAVVWKSVTKNRTSYMR 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      631 TSFSILMSPDSPDPSSLLGILLDIISYVGVGFSILSLAACLVVEAVVWKSVTKNRTSYMR 690

Qy      61 HTCIVNIAASLLVANTWFIIVAAIQDNRYILCKTACVAATFFIHFFYLSVFFWMLTLGLM 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      691 HTCIVNIAASLLVANTWFIIVAAIQDNRYILCKTACVAATFFIHFFYLSVFFWMLTLGLM 750

Qy      121 LFYRLVFILHETSRSTQKAIAFCLGYGCPLAISVITLGATQPREVYTRKINVCWLNWEDTK 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      751 LFYRLVFILHETSRSTQKAIAFCLGYGCPLAISVITLGATQPREVYTRKINVCWLNWEDTK 810

Qy      181 ALLAFAIPALIIVVVNITITIVVITKILRPSIGDKPCKQEKSSLFQISKSIGVLTPLLGL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      811 ALLAFAIPALIIVVVNITITIVVITKILRPSIGDKPCKQEKSSLFQISKSIGVLTPLLGL 870

Qy      241 TWGFGLTTVFPGTNLVFIIFAILNVFQGLFILLFGCLWDLKVQEALLNKFSLSRWSSQH 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      871 TWGFGLTTVFPGTNLVFIIFAILNVFQGLFILLFGCLWDLKVQEALLNKFSLSRWSSQH 930

Qy      301 SKSTSLGSSTPVFSMSSPISRFRNNLFGKTGTYNVSTPEATSSSLENSSSASSLLN 356
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      931 SKSTSLGSSTPVFSMSSPISRFRNNLFGKTGTYNVSTPEATSSSLENSSSASSLLN 986

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